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FIGURE 1

CTAAAAAAATATGTTCTCTACAACACCAAGGCTCATTAATATTTAAATATT
AATATACATTCTTCTGTCAGAAATACATAAAACTTATTATATCAGCGCAGG
GCGGCGCGCGTCGGTCCCAGGAGCAGAACCCGGCTTTCTGGAGCGACG
CTGTCTCTAGTCGCTGATCCAAATGCACCGGCTCATCTTGTCTACACTCTA
ATCTGCGCAAACCTTGCAGCTGTCGGGACACTCTGCAACCCCGCAGAGCG
CATCCATCAAAGCTTGCAGCAGAACCTCAGGCGAGATGAGAGCAATCA
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGGAAACGG
CTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAGGAACCTGCTCCTG
ACATGGCGGCTCACTCTCAGGAGAATACACGGATACAGCTAGTGTGACA
ATCAGTTGGATTAGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTGT
GGAAGTTGAAGATATATCGAAACCAAGTACCTATTAGAGGACATGGTGT
GGACACAAGGAAGTCCCTCCAAGGATAAAATCAAGAACGAACCAAATTAAA
ATCACATTCAAGTCCGATGACTACTTGTGGCTAACCTGGATTCAAGATTAA
TTATTCTTGCTGGAAGATTCCAACCCCGCAGCAGCTTCAGAGACCAACTGGG
AATCTGTACAAGCTCTATTCAAGGAGTACCTCAATCCAGAGTCATGGCAAGAACAT
GATCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATTGCAAGATTGATA
CAAGTGGAGATCTGCTCAAGTACTTCAATCCAGAGTCATGGCAAGAACAT
TGAGAATATGTATCTGGACACCCCTCGGTATCGAGGCAGGTACATACCATGAC
CGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACA
GTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAACAGAGCTGAAGTTGGC
CAATGTGGTCTTCTTCCACGTTGCCTCGTGCAGCGCTGTGGAGGAAATT
GTGGCTGTGGAAGTGTCAACTGGAGGTCTGCACATGCAATTCAAGGAAAC
CGTAAAAAGTATCATGAGGTATTACAGTTGAGCCTGGCACATCAAGAGG
AGGGGTAGAGCTAACGACATGGCTCTAGTTGACATCCAGTTGGATACCCATG
AACGATGTGATTGTATCTGCAGCTCAAGACCACTCGATAAGAGAACATGTGCA
CATCCTACATTAAGCCTGAAAGAACCTTAAAGGAGGGTGAGATAAG
AGACCCCTTCCTACCAGCAACCAAACCTACTAGCCTGCAATGCAATGA
ACACAAGTGGTTGCTGAGTCTCAGCCTGCTTGTAAATGCCATGGCAAGTAG
AAAGGTATATCATCAACTCTATACCTAACGAAATATAGGATTGCATTAAATAAT
AGTGTGAGGTATATATGCAAAACACACACAGAAATATATTGATGTCTAT
GTGTATATAGATCAAATGTTTTGGTATATATAACCAGGTACACCAGAGC
TTACATATGTTGAGTTAGACTCTTAAACCTTGCCTGCAAAATAAGGGATGGT
CAAATATATGAAACATGTCTTAGAAAATTAGGAGATAAAATTATTTAAA
TTTGAAACACAAAACAATTGAAATCTGCTCTTAAAGAAAGCATCTTGT
ATATTAAAAATCAAAAGATGAGGCTTCTTACATATACATCTTAGTTG (SEQ
ID NO:50)



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Figure 2A

1 CTA.....ATATGTTCTCTACAACACCAAGGCTCATTA.....ATTT
46 TAAATATTAATATACATTCTCTGTCAAGAAATACATAAAAACTTT
5 ATTATATCAGCGCAGGGCGGCGGGCGTCGGTCCCAGGACAGAA
136 CCCGGCTTTCTTGAGCGACGCTGTCTCTAGCGCTGATCCCA
181 AATGCACCGGCTCATCTTGCTACACTCTAAATCTGGCGAAACTT
Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe
10 226 TTGCAGCTGTCGGGACACTTCTGCAACCCCCGAGAGCGCATCCAT
Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile
271 CAAAGCTTGCGCAACGCCAACCTCAGGGAGATGAGAGCAATCA
15 Lys Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His
316 CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAAGG
Leu Thr Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly
361 AAACGGCTACGTGCAGAGTCTAGATTCCGAAACAGCTACCCAG
20 Asn Gly Tyr Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg
406 GAACCTGCTCCTGACATGGCGGCTTCACTCTCAGGAGAATACAG
Asn Leu Leu Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg
25 451 GATACAGCTAGTGTTGACAATCAGTTGGATTAGAGGAAGCAGA
Ile Gln Leu Val Phe Asp Asn Gln Phe Gly Leu Glu Glu Ala Glu
496 AAATGATACTGTAGGTATGATTGTGGAAAGTTGAAGATAATAC
30 Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Asp Ile Ser
541 CGAAACCAAGTACCAATTATTAGAGGACGATGGTGTGGACACAAAGGA
Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly His Lys Glu
35 586 AGTTCCCAAGGATAAAATCAAGAACGAAACCAATTAAAATCAC
Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys Ile Thr
631 ATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAAGAT



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PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle

Figure 2B

676 TTATTATTCTTGCTGGAAGATTCACACCCGCAGCAGCTTCAGA
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaAlaSerGlu
5

721 GACCAACTGGGAATCTGTCACAAGCTCTATTCAGGGGTATCCTA
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

766 TAACTCTCCATCAGTAACGGATCCCACCTCTGATTGCGGATGCTCT
10 AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAAATGCAGAATTGATAACAGTGGAAAGATCTGCTCAA
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

856 GTACTTCAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTA
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr
15

901 TCTGGACACCCCTCGGTATCGAGGCAGGTCAATACCATGACCGGAA
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys
20

946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

991 CAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCT
25 SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCAATGTGGCTTCTTCCACGTTGCCTCCTCGTGCA
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln
30

1081 GCGCTGTGGAGGAATTGTGGCTGTGGAACTGTCAACTGGAGGTC
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCACATGCAATTCAAGGAAACCGTGAAAAAGTATCATGAGGT
CysThrCysAsnSerGlyLysThrValLysIleTyrHisGluVal
35

1171 ATTACAGTTGACCCCTGGCCACATCAGACGGACGGCTAGAGCTAA
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys



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1216 GACCATGGCTCTAGTTGACATCCAGTTGGATCACCATGAACGATG
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAAGAGAATGTGCA
5 AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

1306 CATCCTTACATTAAGCCTGAAAGAACCTTGTAGTTAAGGAGGGTG

1351 AGATAAGAGACCCTTTCTACCAAGCAACCAAACCTACTACTAGC

1396 CTGCAATGCAATGAACACACAAGTGGTTGCTGAGTCTCAGCCTTGCT

10 1441 TTGTTAATGCCATGGCAAGTAGAAAGGTATATCATCAACTTCTAT

1486 ACCTAAGAATATAGGATTGCATTTAATAATAGTGTGAGGTTAT

1531 ATATGCACAAACACACACAGAAATATATTATCATGTCTATGTGTATA

1576 TAGATCAAATGTTTTTTGGTATATATAACCAGGTACACCAGAG

1621 CTTACATATGTTGAGTTAGACTCTAAATCCTTGCCAAAATA

15 1666 AGGGATGGTCAAATATATGAAACATGTCTTTAGAAAATTTAGGAG

1711 ATAAATTTATTTTAAATTTGAAAACACAAAACAATTGTGAATCT

1756 TGCTCTCTAAAGAAAGCATCTGTATATTAAAAATCAAAAGATG

1801 AGGCTTTCTTACATATACATCTTAGTTG (SEQ ID NO:50)

Figure 2C



FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCAACTCAGAACCTATAACATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTA
GTAGTAGTAGTAACATATACTACGCAGACTCAGTGAAGGGCCGATTCAACCCT
CTCCAGAGACAACGCCAAGAACACTCACTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATATTACTGTGCGAGAGATATTATGATTACGTTG
GGGAATTATCGCCTCGTTCTACTTGACTACTGGGCCAGGGAACCCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

EVQLVESGGGLVKPGGSLRLSCAASGFNFRTYNMNWVRQAPGKGLEWVSSISSS
SSNIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIAS
FYFDYWQGTLTVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TTTCAGCAGAAACCAGGGAAAGCCCCATAAGCCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATAAGGTTCAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGCTACTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWFQQKPGKAPKRLIYASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKEIK (SEQ
ID NO:14)



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FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGGAGGCTTGATCCAGCCTGGGGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGC
TGGGTCCGCCAGGCTCCAGGGAAAGGGGCTGGAGTGGGTCTCAGTTATTATA
GCGGTGGTAGCACATACTACCGCAGACTCCGTGAAGGGCCGATTCACCATCTC
CAGAGACAATTCCAAGAACACCGCTGTATCTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCCGTGTATTACTGTGCAGGAAACGGTACTACGAATTACTACT
ACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

EVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG
GSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTNYYGM
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCAAAGTAATGGATAC
AACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTCACAGCTCCTGA
TCTATTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCACTGGCAGT
GGATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG
TTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCTCACTTCGGCGGAGGG
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

DIVMTQSPLSLPVTPGEPAISCRSSQSLLQSNGNYLDWYLQKPGQSPQLLIYLG
SNRASGVPDRFSGSGSTDFTLKISRVEAEDVGVYYCMQALQTLFGGGTKVEI
K (SEQ ID NO:16)



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FIGURE 5

A -- Cur2 1.17 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGT
ATGATGGAAGTAATAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAACAGCCTGAGA
GCCGAGGGACACGGCTGTGTATTACTGTGCGAGAGATCAAGGATACAGATATG
CTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCCTCCTCAG (SEQ ID NO:59)

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYA
GYYDYGMDVWQGQGTTVTVSS (SEQ ID NO:17)

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCCTAACGGTTAACGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTATTACT
GTCTACAGCATAATAGTTACCCGCTACTTCGGCGGAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:60)

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKVEIK (SEQ
ID NO:18)



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FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCAAACAGTGGTAACACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGAGGGTATAGCAGTGGC
TGGGACATACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:61)

B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAG
YYYYYYGMDVWGQGTTVTVSS (SEQ D NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACAGGTTAGCAGCGCCTGATCTATGCTGCATCCA
GTTTGCAGAAAGTGGGGTCCCCTAACAGGTTAGCAGCGCAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTCT
GTCTACAGCATAATAGTTACCCATTCACTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:62)

D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ
ID NO:20)



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FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAAC
CCTAACAGTGGTAACACAGGCTATGCACAGAAAGTCCAGGGCAGAGTCACCA
TGACCAGGAACACCTCCATAAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTG
GGGGAGTTATCGTGCACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACGCGCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCCTAACAGGTTCAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT
GTCTACAGCATAATAGTGACCCGTGCAGTTGGCCAGGGACCAAGCTGGA
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTDFLTISLQPEDFATYYCLQHNSDPCSFGQGTKLEIR (SEQ
ID NO:22)



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FIGURE 8

A -- Cur2 1.23 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGGAGTCT
CTGAAGATCTCCTGTGAGGGTTCTGGATACAGCTTACCAAGCTACTGGATCGG
CTGGGTGCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTGACTCTGATACCAAGATAACAGACAGCCCCTCCCAAGGCCAGGTACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCAGACATGTATCGTATTACTATG
TTTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGVТИADKSISTAYLQWSSLKASDTAMYCARHVSYYVSGS
YYNVFDYWGQGTLVTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGATACCAGGGAAAGCCCCTAACGCGCCTGATCTATGCTGCATCCA
GTTTGCAACGTGGGGTCCCATCAAGGTTCAAGCAGCGGAGTGGATCTGGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR
GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:24)



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FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTCAAGTTCAAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGT
ATGATGGAAGTAATAAAATACTATGCAGACTCCGTGAAGGGCCGATTCAACCCT
CTCCAGAGACAATTCCAAGAACACCGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTATTATTGTGCGAGAGATCAGGGATACAGCTATG
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCAG (SEQ ID NO:67)

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGVVQPGRLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYG
YVYYDYGMDVWGQGTTVTVSS (SEQ ID NO:25)

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTTGCAGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGA
GTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTCGAACCTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:68)

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:26)



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FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

```
GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCAGGGAGTCT
CTGAAGATCTCCTGTAAGGGTCTGGATACAGGTTACCACTGGATCGG
CTGGGTGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTACTCTGATACAGATAACAGCCCCTACCTGCAGTGGAGCAGCCTGAA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG
GTTCGGAGACTTATTATAATGCTTGACTACTGGGCCAGGGAACCCCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:69)
```

B -- Cur2 1.25.1 heavy chain protein sequence

```
EVQLVQSGAEVKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPG
DSDTRYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYGSET
YYNVFDYWQGQTLTVSS (SEQ ID NO:27)
```

C -- Cur2 1.25.1 light chain nucleotide sequence

```
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAACGGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCCTAACGGTTCAGCGGCAGTGGATCTGGACAGA
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:70)
```

D -- Cur2 1.25.1 light chain protein sequence

```
DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:28)
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FIGURE 11

A -- Cur2 1.29 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTGAAAAAGCCCAGGGAGTCT
CTGAAGATCTCCTGTAAGGGTCTGGATACAGCTTACCACTGACTGGATCGG
CTGGGTGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTACTCTGATACAGATACAGCCCCTCCTCCAAGGCCAGGCCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGCT
ACGATTGGGGATATTACTATTACTACCACGGTATGGACGTCTGGGCCAAG
GGACCACGGTCACCGTCTCAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG
YYYYYHGMDVWGQGTTVTVSS (SEQ ID NO:29)

C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACA
ACTATTGGATTGGTACCTGCAGAACGCCAGGGCAGTCTCCACAACCTCCTGATC
TATTTGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGTGG
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT
GGGGTTTATTACTGCATGCAAGCTCTACAATCTCATGTGCAGTTGGCCA
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLIYLG
SNRASGPDRFSGSGSTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTLK
EIK (SEQ ID NO:30)



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FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG
CTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCAGAGATCATTACTATGATAGT
AGTGATTATCTCTACTACTACGGTTGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDSTSTAYMELRSLSRSDDTAVYYCARDHYYDSS
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCTAAGCTCCTGATCTATGCTGCATCCAC
TTTGCATCAGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGACAGATT
TCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTAACTGT
CAAAAGTATAACAGTGCCCGCTCACTTCGGCGGAGGGACCAAGGTGGAGA
TCAAAC (SEQ ID NO:74)

D -- Cur2 1.33 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQ
SGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNNSAPLTFFGGTKVEIK (SEQ
ID NO:32)



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FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCC
TGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGT
ATGATGGAAATGATAAAACTATGCAGACTCCGTGAAGGGCCGCTTCACCGT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATTACTATGATAGTA
GTGATTATCTCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC
GGTCACCGTCTCCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

QVQLVESGGVVQPGRLSRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAAIWIY
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS
DYLYYYYYGMDVWQGTTVTVSS (SEQ ID NO:33)

C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCGAGTCAGGGCATTAGCAATTATTCAGCCTGGT
ATCAGCAGAAACCAGGGAAAGTTCTAACCTCCTGATCTATGCTGCATCCAC
TTTGCAATCAGGGGTCCCATCTCGGTTAGTGGCAGTGGATCTGGACAGATT
TCTCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAGCTTATTACTGT
CAAAAGTGTAAACAGTGCCCCGTGGACGTTGGCCAAGGGACCACGGTGGAG
ATCAAAC (SEQ ID NO:76)

D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ
SGVPSRFSGSGETDFSLTISSLQPEDVAAYYCQKCNSAPWTFGQGTTVEIK (SEQ
ID NO:34)



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FIGURE 14

A -- Cur2 1.39.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAACAGAGGTGAAAAAGCCCAGGGAGTCT
CTGAAGATCTCCTGTAAGGGTCTGGATACAGGTTACCACTGGATCGG
CTGGGTGCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTGACTCTGATAACAGATAACAGCCGCTTCCAAGGCCAGGTACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA
ATTCGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCTGGTC
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

EVQLVQSGTEVKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIYPG
DSDTRYSPSFQGVVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYYNSGS
YYNVFDYWGQGTLVTVSS (SEQ ID NO:35)

C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCTAAGCGCCTGATCTATGCTGCATCCA
GTTTGCAAAGTGGGGTCCCATCAAGGTTAGCGGCAGTGGATCTGGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTATTACT
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:78)

D -- Cur2 1.39.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ
ID NO:36)



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FIGURE 15

A -- Cur2 1.40.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCACTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAATGGATGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCCTAACGACACGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AGCTGCTACCAACTACTAACACGGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCARDIVVVV
AATNYYNGMDVWGQGTTVTVSS (SEQ ID NO:37)



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FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACCAAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA
TGGTTACGACTACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTC
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG
YDYYYGMDVWGQGTTVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCAATTGCCGGCGAGTCAGGGCATTAGCAATGATTAGCCTGG
TATCAGCAGAAACCAGGGAAAGTTCTAACAGCTCCTGATCTATGCTGCATCCA
CTTGCAATTAGGGTCCCCTCTCGGTTAGTGGCAGTGGATCTGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG
TCAAAAGTATAACAGTGCCCCATTCACTTCGGCCCTGGGACCAAAGTGGAT
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ
LGVPSRFSGSQGTDFTLTISLQPEDVATYYCQKYNsapFTFGPGTKVDIK (SEQ
ID NO:39)



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FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGGCTCA
GTGAAGGTCTCTGCAAGGCTCTGGATACTCCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACACAAGGGCTTGAGTGGATGGATGGATGAA
CCCTAACAAATGGTAACACAGGCTATGCACAGAAGTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT
AACTGCTACGGACTACTACCGTATGGACGTCTGGGGCCAAGGGACCACG
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWM
NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT
ATDYYYGMDVWGQGTTVTVSS (SEQ ID NO:40)

C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG
TATCAGCAGAAACCAGGGAAAGCCCCATAAGCGCCTGATTTGCTGCATCCA
GTTGCCAAGTGGGGTCCCCTCAAGGTTAGCGGGCAGTGGATCTGGACAGA
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTACT
GTCTACAGCATAGTGGTACCCCTCCGACGTTCGGCCAAGGGACCAAGGTGGA
AATCAAAC (SEQ ID NO:83)

D -- Cur2 1.46.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLPS
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID
NO:41)



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FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTACCGCTATGGTATCAGC
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG
CTTACAATGGTAACACACAAACTATGCACAGAACAGCTCCAGGGCAGAGTCACCAT
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGATGTTGAATATTACTATG
ATGGTAGTGGTTATTACTACTTTGACTACTGGGCCAGGAAACCCTGGTCACC
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCARDVEYYYD
GSGYYYYFDYWGQGTLVTVSS (SEQ ID NO:42)

C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTGCATCTGTAGGAGACAG
AGTCACCATCACTTGTGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG
TATCAGCAGAAACCAGGGAAAGGCCCTAACGGTCTGATCTATGCTGCATCCA
TTTGCAAAGTGGGGTCCCCTAACGGTCTGAGCGGCAGTGGATCTGGGACAGA
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTGCATCTTACTATT
GTCAACAGTCTAACAGTTCCCTCGGACGTTGGCCAAGGGACCAAGGTGGA
GATCAAAC (SEQ ID NO:85)

D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAA SILQ
SGVPSRFSGSGSGTDFLTISLQPEDFASYYCQQSNSFPRTFGQGTKVEIK (SEQ
ID NO:43)



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FIGURE 19

A -- Cur2 1.49.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTCTGGATACACCTCACCAAGTTATGATATCAA
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA
CCCTAACAGTGGTGACACAGGCTATGCACAGAACAGTCCAGGGCAGAGTCACC
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA
GATCTGAGGACACGGCGTGTATTCTGTGCGAGAATGAGGGATATAGTGGC
TACGAGCTATTACTACTTCTACGGTATGGACGTCTGGGGCCAAGGGACC
ACGGTCACCGTCTCCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM
NPNSGDTGYAQKFQGRVTMRTNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT
YYYYYFYGMDVWGQGTTVTVSS (SEQ ID NO:44)

C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCC
GGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACA
ACTATTGGATTGGTACCTGCTGAAGCCAGGGCAGTCTCCACAGCTCCTGATC
TATTGGGTTCTAGTCGGGCCTCCGGGGTCCCTGACAGGTTAGTGGCAGTGG
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAACACTACAAACTATCACCTTCGGCCAAGGGGA
CACGACTGGAGATTAAAC (SEQ ID NO:87)

D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLHSNGNYLDWYLLKPGQSPQLLIYLG
SSRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQLQTITFGQGTRLEIK
(SEQ ID NO:45)



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FIGURE 20

A -- Cur2 1.51 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTCTGGATACAGCTTACCACTGGATCGG
CTGGGTGCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT
CCTGGTACTCTGATGCCAATACAGCCCCTCCTCCAAGGCCAGGTACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACACTATGATTACGTTGG
GGAATTATCGGTATACAGGGTGGTCGACCCCTGGGCCAGGGAACCTGGT
CACCGTCTCCTCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG
DSDAKYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCARHYDYYWRNY
RYTGWFDPWGQGTLVTVSS (SEQ ID NO:46)

C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTGTCTCCAGGGGAAAG
AGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCAGCTACTTAGCC
TGGTACCAAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAT
CCAACAGGGCCACTGGCATCCCAGACAGGTTAGTGGCAGTGGGTCTGGGAC
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATT
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTCGGCCCTGGGACCAAAGTG
GATATCAAAC (SEQ ID NO:89)

D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASNRA
TGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSLSFTFGPGTKVDIK (SEQ
ID NO:47)



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FIGURE 21

A -- Cur2 6.4 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAGTTATGATATCAAC
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATAAAC
CCTAATAGTGGTAACACAGACTATGCACAGAACAGTTCCAGGGCAGAGTCACCA
TGACCAGGGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG
ATCTGAGGACACGGCCATATATTATTGTGTGAGAGGGCTTGGATACAGCTAT
AATTACGACTACTATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWIN
PNSGNTDYAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY
DYYYGMDVWGQGTTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTGTCCTCCAGGGAAAG
AGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGTAGTTACTTAGCCT
GGTACCAAGCAGAACGCCTGGCCAGGCTCCAGGCTCCTCATCTATGCTACATC
CAGCAGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGGTCTGGGACA
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATTA
CTGTCAGCAGTATGGTAGTTACCGTGCAGTTGGCCAGGGGACCAAGCTG
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRA
TGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSSPCSFQGTLEIK (SEQ
ID NO:49)



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FIGURE 22A

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2		V	D	J	V				D & J		
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0



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FIGURE 22B

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes							
		V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
					V						D & J
CR2		V	D	J							
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	mix									
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1	0/0
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1	0/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1	0/0
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0	0/0
1.51.1	VH	5-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1	0/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2	0/0



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FIGURE 23

Figure 23A

						Section 1
	(1) 1	10	20	30	40	51
CUR2-1.6.1_HC	(1) EVQLVESGGGLVPRGGLRLSCAASGFNFR			Y	MNNWVRQAPGKGLEWVSSI	
VH3-21	(1) EVQLVESGGGLVPRGGLRLSCAASGFTEF			S	MNNWVRQAPGKGLEWVSSI	
Consensus	(1) EVQLVESGGGLVPRGGLRLSCAASGF			F	SY MNWVRQAPGKGLEWVSSI	
						Section 2
	(52) 52	60	70	80	90	102
CUR2-1.6.1_HC	(52) 3333SNIYXADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDIMI					
VH3-21	(52) 3333SYIYXADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAR					
Consensus	(52) 33333 IYYADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAR					
						Section 3
	(103) 103	110	126			
CUR2-1.6.1_HC	(103) TFGGIIIASFYFDYWGQGTIVTVSS					
VH3-21	(99) -----					
Consensus	(103)					

Figure 23B

						Section 1
	(1) 1	10	20	30	40	51
CUR2-1.6.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGW			Q	QKPGKAPKRLIYAA	
A30	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGW			Q	QKPGKAPKRLIYAA	
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGW			P	QKPGKAPKRLIYAA	
						Section 2
	(52) 52	60	70	80	90	102
CUR2-1.6.1_LC	(52) S8LQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP			L	TPGGGT	
A30	(52) S8LQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP			-----		
Consensus	(52) S8LQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYP					
						Section 3
	(103) 103 107					
CUR2-1.6.1_LC	(103) KVEIK					
A30	(96) -----					
Consensus	(103)					



3 10 00 11 1 23 6 13 0 0 0 2 1 2 3 0 0 2
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FIGURE 24

Figure 24A

	Section 1					
	(1) 1	10	20	30	40	51
Cur2-1.11.1_HC	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSNYMSWVRQAPGKGLEWVSVI					
VH3-53	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSNYMSWVRQAPGKGLEWVSVI					
Consensus	(1) EVOLVE8GGGLIOPGGSLRLSCAASGFTVSNYMSWVRQAPGKGLEWVSVI					
	Section 2					
	(52) 52	60	70	80	90	102
Cur2-1.11.1_HC	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
VH3-53	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
Consensus	(52) Y8GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAGTVTTN					
	Section 3					
	(103) 103	110	120			
Cur2-1.11.1_HC	(103) YYQGMDVWGQGTTTVSS					
VH3-53	(98) -----					
Consensus	(103) YYQGMDVWGQGTTTVSS					

Figure 24B

	Section 1					
	(1) 1	10	20	30	40	51
CUR2-1.11.1_LC	(1) DIVMTQSPLSLPVTPGEPAASISCRSSQSLLSNGNYNLDWYLQKPGQSPQL					
A19	(1) DIVMTQSPLSLPVTPGEPAASISCRSSQSLLHNGNYNLDWYLQKPGQSPQL					
Consensus	(1) DIVMTQSPLSLPVTPGEPAASISCRSSQSLL SNGNYNLDWYLQKPGQSPQL					
	Section 2					
	(52) 52	60	70	80	90	102
CUR2-1.11.1_LC	(52) LIYLGSNRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
A19	(52) LIYLGSNRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
Consensus	(52) LIYLGSNRASGVFDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTLTF					
	Section 3					
	(103) 103	111				
CUR2-1.11.1_LC	(103) GGGTKVEIK					
A19	(101) -----					
Consensus	(103) GGGTKVEIK					



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FIGURE 25

Figure 25A

	Section 1				
	(1) 1	10	20	30	40
CR2-1.17.1 HC	(1) QVQLVE3GGGVVQPG	SLRLSCAASGFTFSSYGMHWWVROAPGKGLEWVAI			51
VH3-33	(1) QVQLVE3GGGVVQPG	SLRLSCAASGFTFSSYGMHWWVROAPGKGLEWVAI			
Consensus	(1) QVQLVE3GGGVVQPG	SLRLSCAASGFTFSSYGMHWWVROAPGKGLEWVAI			
	Section 2				
	(52) 52	60	70	80	90
CR2-1.17.1 HC	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY				102
VH3-33	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---				
Consensus	(52) WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR				
	Section 3				
	(103) 103	110	126		
CR2-1.17.1 HC	(103) RYAGYYYYDYGMDVWGQGTTTVSS				
VH3-33	(99) -----				
Consensus	(103)				

Figure 25B

	Section 1				
	(1) 1	10	20	30	40
CR2-1.17.1 LC	(1) DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				52
A30	(1) DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				
Consensus	(1) DIQMTQSPS8L8ASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				
	Section 2				
	(53) 53	60	70	80	90
CR2-1.17.1 LC	(53) S1Q3GVPSRF3GSG3GTETFTLTIS3LQPEDFATYYCLQHNSYP				104
A30	(53) S1Q3GVPSRF3GSG3GTETFTLTIS3LQPEDFATYYCLQHNSYP				
Consensus	(53) S1Q3GVPSRF3GSG3GTETFTLTIS3LQPEDFATYYCLQHNSYP				
	Section 3				
	(105) 1067				
CR2-1.17.1 LC	(105) EIK				
A30	(96) ---				
Consensus	(105)				



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FIGURE 26

Figure 26A

	Section 1					
	(1) 1	10	20	30	40	52
CR2-1.18_HC	(1) QVQLVQSGAEVKRPGAVKVVKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1) QVQLVQSGAEVKRPGAVKVVKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKRPGAVKVVKCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
	Section 2					
	(53) 53	60	70	80	90	104
CR2-1.18_HC	(53) PNSGNTGYAQRKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----					
VH1-8	(53) PNSGNTGYAQRKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----					
Consensus	(53) PNSGNTGYAQRKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR-----					
	Section 3					
	(105) 105	110	126			
CR2-1.18_HC	(105) GTYYYYYYGMDVWGQGTTVTVSS					
VH1-8	(99) -----					
Consensus	(105)					

Figure 26B

	Section 1					
	(1) 1	10	20	30	40	53
CR2-1.18_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS					
	Section 2					
	(54) 54	60	70	80	90	106
CR2-1.18_LC	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATYCLQHNSYEPFTFGPGTKVDI					
A30	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATYCLQHNSYEP-----					
Consensus	(54) LQSGVPSRFSGSGSGTEFTLTISLOPEDFATYCLQHNSYEP-----					
	Section 3					
	(107) 107					
CR2-1.18_LC	(107) K					
A30	(96) -					
Consensus	(107)					



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FIGURE 27

Figure 27A

						Section 1
	(1) 1	10	20	30	40	52
Cur2-1.19.1_hc	(1) QVOLVQSGAEVKKRPGAVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1) QVQIVQSGAEVKKRPGAVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKKRPGAVKV8CKA8GYTFTSYDINWVRQATGQGLEWMGWMN					
						Section 2
	(53) 53	60	70	80	90	104
Cur2-1.19.1_hc	(53) PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCARDVMITY					
VH1-8	(53) PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCAR-----					
Consensus	(53) PNSGNTGYAQKFQGPVTMTRNTSISI8TAYMELSSLRSEDTAVYYCAR					
						Section 3
	(105) 105	110	126			
Cur2-1.19.1_hc	(105) GGVIVHYGMDVWGQGTTVTVSS					
VH1-8	(99) -----					
Consensus	(105)					

Figure 27B

						Section 1
	(1) 1	10	20	30	40	52
Cur2-1.19.1_lc	(1) DIQMTQSPSSILSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAA					
A30	(1) DIQMTQSPSSILSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAA					
Consensus	(1) DIQMTQSPSSILSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRLIYAA					
						Section 2
	(53) 53	60	70	80	90	104
Cur2-1.19.1_lc	(53) S1QSGVPSRF3GSGSGTFTLTISI1QPEDFATYYC1QHN3DFCSFGQGTLK					
A30	(53) S1QSGVPSRF3GEGSGTFTLTISI1QPEDFATYYC1QHN3YF-----					
Consensus	(53) S1QSGVPSRF3GSGSGTDFLTISI1QPEDFATYYC1QHN3P					
						Section 3
	(105) 1067					
Cur2-1.19.1_lc	(105) EIR					
A30	(96) ---					
Consensus	(105)					



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FIGURE 28

Figure 28A

	Section 1				
Cur2-1.23.1_HC VH5-51	(1) 1	10	20	30	40
	(1) EVQLVQSGAABVKRPGESL K ISCE G SGV S FTSYWIGWV R QMPGK G LE W MGII				51
	(1) EVQLVQSGAABVKKPGESL K ISCK G SGY S FTSYWIGWV R QMPGK G LE W MGII				
Consensus	(1) EVQLVQSGAABEVKKPGESL K ISC G SGY S FTSYWIGWV R QMPGK G LE W MGII				
	Section 2				
Cur2-1.23.1_HC VH5-51	(52) 52	60	70	80	90
	(52) YPGDSDTRYSPSFQGQVTISADK S 1 T AYL Q W S SL K A S DT T AMYYCARHV Y				102
	(52) YPGDSDTRYSPSFQGQVTISADK S 1 T AYL Q W S SL K A S DT T AMYYCAR-----				
Consensus	(52) YPGDSDTRYSPSFQGQVTISADK S 1 T AYL Q W S SL K A S DT T AMYYCAR				
	Section 3				
Cur2-1.23.1_HC VH5-51	(103) 103	110	126		
	(103) YYVSGSYNNVFDYWGQGTLTVSS				
	(99) -----				
Consensus	(103)				

Figure 28B

		Section 1				
		10	20	30	40	51
Cur2-1.23.1_LC	(1)	DIQMTQSPSSL	SASVGDRTITCRASQGIRNDLGWYQQIEPGKAPKR	KR	LIYAA	
	A30	(1)	DIQMTQSPSSL	SASVGDRTITCRASQGIRNDLGWYQQIEPGKAPKR	KR	LIYAA
	Consensus	(1)	DIQMTQSPSSL	SASVGDRTITCRASQGIRNDLGWYQQ	PGKAPKR	LIYAA
		Section 2				
Cur2-1.23.1_LC	(52)	SSBLQRGVP	SRFSGSGSGTEFT	LT	TISSILQPFEDPATYYCLOHNSYPWTF	GQGT
	A30	(52)	SSBLQSGVP	SRFSGSGSGTEFT	LT	TISSILQPFEDPATYYCLOHNSYP-----
	Consensus	(52)	SSBLQ	GVP	SRFSGSGSGTEFT	LT
		Section 3				
Cur2-1.23.1_LC	(103)	103	107			
	A30	(103)	KVEIK			
	Consensus	(96)	-----			



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FIGURE 29

Figure 29A

	Section 1				
	1	10	20	30	40
CR2-1.24.1_HC	(1)	QVQLVESGGGVVQPGRLSRLSCAASGF	FSSYGMHWVROAPGKGLEWVADI		51
VH3-33	(1)	QVQLVESGGGVVQPGRLSRLSCAASGF	FSSYGMHWVROAPGKGLEWVAVI		
Consensus	(1)	QVQLVESGGGVVQPGRLSRLSCAASGF	FSSYGMHWVROAPGKGLEWVA	I	
	Section 2				
	52	60	70	80	90
CR2-1.24.1_HC	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGY			102
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	---		
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR			
	Section 3				
	103	110	126		
CR2-1.24.1_HC	(103)	SYGYVYYDYGMDVWGQGTTVTVSS			
VH3-33	(99)	-----			
Consensus	(103)				

Figure 29B

	Section 1				
	1	10	20	30	40
CR2-1.24.1_LC	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPRKLIYAA			52
A30	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPRKLIYAA			
Consensus	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPRKLIYAA			
	Section 2				
	53	60	70	80	90
CR2-1.24.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDPATYYCLQHN3XPWTFGQGTV			104
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDPATYYCLQHN3YP	-----		
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDPATYYCLQHN3YP			
	Section 3				
	105	1067			
CR2-1.24.1_LC	(105)	EIK			
A30	(96)	---			
Consensus	(105)				



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FIGURE 30

Figure 30A

						Section 1
	(1)	10	20	30	40	51
VH5-51	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYSEFTSYWIGWVRQMPGKGLEWMGII				
CR2-1.25.1_HC	(1)	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPGESLKISCKGSGY FTSYWIGWVRQMPGKGLEWMGII				
						Section 2
	(52)	52	60	70	80	90
VH5-51	(52)	YPPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---				102
CR2-1.25.1_HC	(52)	YPPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSY				
Consensus	(52)	YPPGDSDTTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR				
						Section 3
	(103)	103	110	126		
VH5-51	(99)	---				
CR2-1.25.1_HC	(103)	YYGSETYYNVFDYWGQGTLTVSS				
Consensus	(103)	YYGSETYYNVFDYWGQGTLTVSS				

Figure 30B

						Section 1
	(1)	10	20	30	40	52
A30	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				
CR2-1.25.1_LC	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				
Consensus	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAA				
						Section 2
	(53)	53	60	70	80	90
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-----				104
CR2-1.25.1_LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGKTV				
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP				
						Section 3
	(105)	1067				
A30	(96)	---				
CR2-1.25.1_LC	(105)	EIK				
Consensus	(105)	EIK				



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FIGURE 31

Figure 31A

	Section 1					
	(1) 1	10	20	30	40	52
VH5-51	(1) EVQLVQSGAEVKKPGE S LIKISCKGSGYSFTS Y WIGWVRQMPGKGLEWMGIY					
CR2-1.29_HC	(1) EVQLVQSGAEVKKPGE S LIKISCKGSGYSFTS Y WIGWVRQMPGKGLEWMGIY					
Consensus	(1) EVQLVQSGAEVKKPGE S LIKISCKGSGYSFTS Y WIGWVRQMPGKGLEWMGIY					
	Section 2					
	(53) 53	60	70	80	90	104
VH5-51	(53) PGDSLTRYSPSFQGOVTISADRSISTAYLQWSSLKASDTAMYYCAR-----					
CR2-1.29_HC	(53) PGDSLTRYSPSFQGOATISADKSISTAYLQWSSLKASDTAMYYCARHVDVGA					
Consensus	(53) PGDSLTRYSPSFQGO T TISADKSISTAYLQWSSLKASDTAMYYCAR					
	Section 3					
	(105) 105	110	129			
VH5-51	(99) -----					
CR2-1.29_HC	(105) TIGGYYYYYHGMDVWGQGTTVTVSS					
Consensus	(105)					

Figure 31B

	Section 1					
	(1) 1	10	20	30	40	53
A19	(1) DIVMTQSP L SLPV T GE P AS I SCR S Q S LLH S NG N YLDW Y LQKPGQSPQLLI					
CR2-1.29_LC	(1) DIVMTQSP L SLPV T GE P AS I SCR S Q S LLH S NG N YLDW Y LQKPGQSPQLLI					
Consensus	(1) DIVMTQSP L SLPV T GE P AS I SCR S Q S LLH S NG N YLDW Y LQKPGQSPQLLI					
	Section 2					
	(54) 54	60	70	80	90	106
A19	(54) YLGSNRASGV P DRFSGSGSGTDFTLKISRVEA D VGVYYCMQALQ P -----					
CR2-1.29_LC	(54) YLGSNRASGV P DRFSGSGSGTDFTLKISRVEA D VGVYYCMQALQ L MC S F G Q					
Consensus	(54) YLGSNRASGV P DRFSGSGSGTDFTLKISRVEADDVGVYYCMQALQ S					
	Section 3					
	(107) 107	113				
A19	(101) -----					
CR2-1.29_LC	(107) G T KLEI R					
Consensus	(107)					



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FIGURE 32

Figure 32A

	Section 1				
	(1) 1	10	20	30	40
VH1-18	(1) QVQLVQSGAEVRRPGASVVKVSKCASGTYFTSYGI SWVRQAPGQGLEWMGWIS				
CR2-1.33_HC	(1) QVQLVQSGAEVKKPGASVVKVSKCASGTYFTSYGI SWVRQAPGQGLEWMGWIS				
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSKCASGTYFTSYGI SWVRQAPGQGLEWMGWIS				
	Section 2				
	(53) 53	60	70	80	90
VH1-18	(53) AYNGNTNYAOKLQGRVTMTTD TSTSTAYMELRSIRSDDTAVYYCAR				
CR2-1.33_HC	(53) AYNGNTNYAOKLQGRVTMTTD TSTSTAYMELRSIRSDDTAVYYCARDHYYDS				
Consensus	(53) AYNGNTNYAOKLQGRVTMTTD TSTSTAYMELRSIRSDDTAVYYCAR				
	Section 3				
	(105) 105	110	127		
VH1-18	(99) -----				
CR2-1.33_HC	(105) SDYLYYYYYGLDVWGQGTTVTVSS				
Consensus	(105)				

Figure 32B

	Section 1				
	(1) 1	10	20	30	40
A20	(1) DIOMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVKPLLIYAAST				
CR2-1.33_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVKPLLIYAAST				
Consensus	(1) DIOMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVKPLLIYAAST				
	Section 2				
	(54) 54	60	70	80	90
A20	(54) DQSGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYN SAP				
CR2-1.33_LC	(54) DQSGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYN SAPLTFGGGTKVEI				
Consensus	(54) DQSGVPSRFSGSGSGTDFLTISLQPEDVATYYCQKYN SAP				
	Section 3				
A20	(107) M7				
A20	(96) -				
CR2-1.33_LC	(107) K				
Consensus	(107)				



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FIGURE 33

Figure 33A

		Section 1									
		10	20	30	40	50					
VH3-33	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
CR2-1.38.1_HC	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
	(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA				
Consensus		(1)	QVQLVE	GGGVVQPGRA	SIRLSCAASGFTF	SSYGMH	WVRQAPGK	GLEWVAA			
Section 2											
		52	60	70	80	90					
VH3-33	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
CR2-1.38.1_HC	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
	(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---		
Consensus		(52)	WYDGSNKYYAD	SVKGRFTI	SRDN	SKNTLYLQ	MNSLRA	EDTAV	YYCAR	---	
Section 3											
		103	110	127							
VH3-33	(99)	-----	-----	-----							
	(103)	DSSDYL	YYYYGMDV	WGQGTT	TVSS						
	(103)	DSSDYL	YYYYGMDV	WGQGTT	TVSS						
CR2-1.38.1_HC		(103)	DSSDYL	YYYYGMDV	WGQGTT	TVSS					
Consensus		(103)	DSSDYL	YYYYGMDV	WGQGTT	TVSS					

Figure 33B



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FIGURE 34

Figure 34A

	1	10	20	30	40	51	Section 1
VH5-51	(1)						
CR2-1.39.1_HC	(1)	EVOLVQSGAEVKRPGESELKISCKGSGYSPFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1)	EVQLVQSGTEVKRPGESELKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII					
	(1)	EVQLVQSG	EVKKPGESLKIISCKGSGY	FTSYWIGWVRQMPGKGLEWMGII			Section 2
	52	60	70	80	90	102	
VH5-51	(52)	YPCGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---					
CR2-1.39.1_HC	(52)	YPCGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSY					
Consensus	(52)	YPCGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					Section 3
	103	110	126				
VH5-51	(103)	(99)	-----				
CR2-1.39.1_HC	(103)	YYNSGSYYNVFDYWGQGTLTVSS					
Consensus	(103)						

Figure 34B

	1	10	20	30	40	52	Section 1
A30	(1)						
CR2-1.39.1_LC	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAPKRLIYAS					
Consensus	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAPKRLIYAS					
	(1)	DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAPKRLIYAS					Section 2
	53	60	70	80	90	104	
A30	(53)	SLQ3GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP-----					
CR2-1.39.1_LC	(53)	SLQ3GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKV					
Consensus	(53)	SLQ3GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP					Section 3
	105	1087					
A30	(105)	(96)	---				
CR2-1.39.1_LC	(105)	EIK					
Consensus	(105)						



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FIGURE 35

Figure 35A

						Section 1
VH1-8	(1) 1	10	20	30	40	52
CR2-1.45_HC	(1) QVQLVQSGAEVKREGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMN					
						Section 2
VH1-8	(53) 53	60	70	80	90	104
CR2-1.45_HC	(53) PNSGNTGYAQQKPGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR-----					
Consensus	(53) PNSGNTGYAQQKPGQGRVTMTRNTSISTAYMELSSLRSED TAVYYCAR-----					
						Section 3
VH1-8	(105) 105	110	125			
CR2-1.45_HC	(105) GYDYYYGMDVWGQGTTVTVSS					
Consensus	(105)					

Figure 35B

						Section 1
A20	(1) 1	10	20	30	40	53
CR2-1.45_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGINSNYLAWYQQKPGKVPKLLIYAAST					
Consensus	(1) DIQMTQSPSSLSASVGDRVTI CRASQGINSN LAWYQQKPGKVPKLLIYAAST					
						Section 2
A20	(54) 54	60	70	80	90	106
CR2-1.45_LC	(54) DQSGVE3RF3GSGSGTDFTLTISLQPED VATYYCQKYN SAP-----					
Consensus	(54) DQLGVE3RF3GSGSGTDFTLTISLQPED VATYYCQKYN SAPFTFGPGTKVDI					
						Section 3
A20	(107) 107					
CR2-1.45_LC	(107) K					
Consensus	(107)					



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FIGURE 36

Figure 36A

	Section 1				
	(1) 1	10	20	30	40
VH1-8	(1) QVQLVQSGAEVKKPGASVVKVSCKASGY		FTSYDINWVRQATGQGLEWMGWM		
CR2-1.46.1_HC	(1) QVQLVQSGAEVKKPGASVVKVSCKASGY		FTSYDINWVRQATGQGLEWMGWM		
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWM				
	Section 2				
	(52) 52	60	70	80	90
VH1-8	(52) NPNSGNTGYAQKFOGRVMTMTRNTSISTAYMELSSLRSEDTAVYYCAR				102
CR2-1.46.1_HC	(52) NPNNGNTGYAQKFOGRVMTMTRNTSISTAYMELSSLRSEDTAVYYCAR				IVV
Consensus	(52) NPN GNTGYAQKFOGRVMTMTRNTSISTAYMELSSLRSEDTAVYYCAR				
	Section 3				
	(103) 103	110	126		
VH1-8	(99) -----				
CR2-1.46.1_HC	(103) VVTATDYYYGMDVWGQGTTVTVSS				
Consensus	(103)				

Figure 36B

	Section 1				
	(1) 1	10	20	30	40
A30	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNLGLGWYQQKPGKAPKRLI				52
CR2-1.46.1_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNLGLGWYQQKPGKAPKRLI				AAS
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNLGLGWYQQKPGKAPKRLI				AAS
	Section 2				
	(53) 53	60	70	80	90
A30	(53) SLOQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYYCLQHNSYP				104
CR2-1.46.1_LC	(53) SLP3GVPSRF3GSGSGTEFTLTISISSLQPEDFATYYCLQHSGYPPTFGQGTV				
Consensus	(53) SL SGVPSRFSGSGSGTEFTLTISISSLQPEDFATYYCLQH YP				
	Section 3				
	(105) 105				
A30	(96) ---				
CR2-1.46.1_LC	(105) EIK				
Consensus	(105)				



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FIGURE 37

Figure 37A

						Section 1
	(1)	10	20	30	40	51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKEPGASVVKVSCKASGYTFTS/GTISWVROAEPGOGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKEPGASVVKVSCKASGYTFTS/YGTISWVROAEPGOGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKEPGASVVKVSCKASGYTFTS/YGTISWVROAEPGOGLEWMGWI				
						Section 2
	(52)	52	60	70	80	90
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVIMTTDTSTSTAYMELRSLRSDDTAVYYCARDVEY				102
VH1-18	(52)	SAYNGNTNYAQKLQGRVIMTTDTSTSTAYMELRSLRSDDTAVYYCAR---				
Consensus	(52)	SAYNGNTNYAQKLQGRVIMTTDTSTSTAYMELRSLRSDDTAVYYCAR				
						Section 3
	(103)	103	110	125		
CR2-1.48.1_HC	(103)	YYDGSGYYYYFDYWGQGTIVTVSS				
VH1-18	(99)	-----				
Consensus	(103)					

Figure 37B

						Section 1
	(1)	10	20	30	40	52
CR2-1.48.1_LC	(1)	DIQMTQSPESVSVASVGDRVTITCRASQGISESWLAWYQQKEGKAPKLLIYAA				
L5	(1)	DIQMTQSPESVSVASVGDRVTITCRASQGISESWLAWYQQKEGKAPKLLIYAA				
Consensus	(1)	DIQMTQSPESVSVASVGDRVTITCRASQGISESWLAWYQQKEGKAPKLLIYAA				
						Section 2
	(53)	53	60	70	80	90
CR2-1.48.1_LC	(53)	ILQSGVPSRFQSGSGTDFTLTISIQLQPEDFA	YYCQQ	NSFPRTFGQGTV		104
L5	(53)	SLQ3GVPSRFQSGSGTDFTLTISIQLQPEDFA	YYCQQ	NSFP-----		
Consensus	(53)	ILQSGVPSRFQSGSGTDFTLTISIQLQPEDFA	YYCQQ	NSFPANSFP		
						Section 3
	(105)	1067				
CR2-1.48.1_LC	(105)	EIR				
L5	(96)	---				
Consensus	(105)					



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FIGURE 38

Figure 38A

	1	10	20	30	40	51	Section 1
CR2-1.49.1_HC	(1) QVQLVQSGA V KP G ASV K V S CKA S GY T FT S Y D IN W V R AT G Q G LEWM G WM						
VH1-8	(1) QVQLVQSGA V R K E G ASV K V S CKA S GY T FT S Y D IN W V R AT G Q G LEWM G WM						
Consensus	(1) QVQLVQSGA E V K KP G ASV K V S CKA S GY T FT S Y D IN W V R AT G Q G LEWM G WM						
	52	60	70	80	90	102	Section 2
CR2-1.49.1_HC	(52) N E NSG D T G Y A Q K P G R V T M T P NT S I S T A Y M E L S S L R SE T A V Y C ARM R DI						
VH1-8	(52) N E NSG G N T G Y A Q K P G R V T M T P NT S I S T A Y M E L S S L R SE T A V Y C AR ---						
Consensus	(52) N E NSG G T G Y A Q K F Q G R V T M T NT S I S T A Y M E L S S L R SE T A V Y F C AR						
	103	110	127				Section 3
CR2-1.49.1_HC	(103) VAT S Y Y Y F Y G MD V W G Q T T V S						
VH1-8	(99) -----						
Consensus	(103)						

Figure 38B

	1	10	20	30	40	52	Section 1
CR2-1.49.1_LC	(1) D I VM T Q S P L S LP V T P GE P A S I S CR S S Q S L L H S N G Y N Y L D W Y L K P G Q S P O L L						
A19	(1) D I VM T Q S P L S LP V T P GE P A S I S CR S S Q S L L H S N G Y N Y L D W Y L K P G Q S P O L L						
Consensus	(1) D I VM T Q S P L S LP V T P GE P A S I S CR S S Q S L L H S N G Y N Y L D W Y L K P G Q S P O L L						
	53	60	70	80	90	104	Section 2
CR2-1.49.1_LC	(53) IYLG S RAS G V P DR P S G S G T L F T L K I S R V E A E D V G V Y Y C M O T I Q T I T F G Q						
A19	(53) IYLG S RAS G V P DR P S G S G T L F T L K I S R V E A E D V G V Y Y C M O A I Q T F ---						
Consensus	(53) IYLG S RAS G V P DR P S G S G T D F T L K I S R V E A E D V G V Y Y C M Q I Q T -----						
	105	111					Section 3
CR2-1.49.1_LC	(105) G T R L E I K						
A19	(101) -----						
Consensus	(105)						



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FIGURE 39

Figure 39A

	Section 1					
	(1) 1	10	20	30	40	51
CR2-1.51.1_HC	(1) EVOLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII					
VH5-51	(1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1) EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII					
	Section 2					
	(52) 52	60	70	80	90	102
CR2-1.51.1_HC	(52) YPGDSDA	YSPSFQGQVTISADKSISTAYLQWSSILKASDTAMYYCARHYDY				
VH5-51	(52) YPGDSDT	YSPSFQGQVTISADKSISTAYLQWSSILKASDTAMYYCAR---				
Consensus	(52) YPGDSD	YSPSFQGQVTISADKSISTAYLQWSSILKASDTAMYYCAR				
	Section 3					
	(103) 103	110	126			
CR2-1.51.1_HC	(103) VWRNYRYTGWFDPWQGQTLTVTVSS					
VH5-51	(99) -----					
Consensus	(103)					

Figure 39B

	Section 1					
	(1) 1	10	20	30	40	52
CR2-1.51.1_LC	(1) EIVLTOQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
A27	(1) EIVLTOQSPGTLSLSPGERATLSCRABOSVSSSYLAWYQQKPGQAPRLLIYGA					
Consensus	(1) EIVLTOQSPGTLSLSPGERATLSCRASQSVSSESYLAWYQQKPGQAPRLLIYGA					
	Section 2					
	(53) 53	60	70	80	90	104
CR2-1.51.1_LC	(53) S R ATGIPDRFSGSGSGT L T L T I S R LEPEDFAVYYCQQYGSSLFTP PG TK					
A27	(53) S R ATGIPDRFSGSGSGT D FT L T I S R LEPEDFAVYYCQQYGSSP-----					
Consensus	(53) S RATGIPDRFSGSGSGT D FT L T I S R LEPEDFAVYYCQQYGSS					
	Section 3					
	(105) 10508					
CR2-1.51.1_LC	(105) VDIK					
A27	(97) -----					
Consensus	(105)					



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FIGURE 40

Figure 40A

	(1) 1	10	20	30	40	52	Section 1
Cur2-6.4.1 hc	(1) QVQLVQSGAEVKREGASVVKVSKAKASGYMPTSYDINWVRQATGGGLEWMGW						
VH1-8	(1) QVQLVQSGAEVKREGASVVKVSKAKASGYTFTSYDINWVRQATGGGLEWMGW						
Consensus	(1) QVQLVQSGAEVKPGASVVKVSKAKASGYTFTSYDINWVRQATGGGLEWMGW						
	(53) 53	60	70	80	90	104	Section 2
Cur2-6.4.1 hc	(53) PNSGNTDYAQKFQGRVTMTRDTTSISTAYMELSSRLSEDTA						
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSRLSEDTA						
Consensus	(53) PNSGNT YAQKFQGRVTMTR TSISTAYMELSSRLSEDTAIYYC R						
	(105) 105	110	125				Section 3
Cur2-6.4.1 hc	(105) NYDYYYYGMDVWGQGTTVTVSS						
VH1-8	(99) -----						
Consensus	(105)						

Figure 40B

	(1) 1	10	20	30	40	52	Section 1
Cur2-6.4.1 Lc	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYT						
A27	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA						
Consensus	(1) EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYA						
	(53) 53	60	70	80	90	104	Section 2
Cur2-6.4.1 Lc	(53) S9RATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS93FCSFGQG						
A27	(53) S9RATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS93FCSFGQG						
Consensus	(53) S9RATGIPDRFSGSGSGTDFTLTISRLPELFAYYYCQQYGS93FCSFGQG						
	(105) 10508						Section 3
Cur2-6.4.1 Lc	(105) LEIK						
A27	(97) ---						
Consensus	(105)						

CLONE #	VH	#DB L	VH END	# N's Sequence	DH	Size of D	D Sequence	# N's Sequence	JH # del	JH segment
1.19. 1	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
1.19. 2	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
1.19. 3	DP-15/1- 8	-1	CGAGAG (SEQ ID NO:92)	3 ACG	D3-16	28	TTATGATTACGTT GGGGGAGTTATCGT (SEQ ID NO:93)	2 GC	JH6 B	-12 ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6 0	ATTACTAC (SEQ ID NO:97)
6.4.2	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6 0	ATTACTAC (SEQ ID NO:97)
6.4.3	DP-15/1- 8	0	GAGAGG (SEQ ID NO:95)	3 CTT	D5-18	12	TGGTACAGCTA (SEQ ID NO:96)	2 TA	JH6 0	ATTACTAC (SEQ ID NO:97)

CLONE	VK	#de 1	VK end	#n	N SEQ	JK	# del	JK end
1.19. 1	A3.0	-3	TTACCC (SEQ ID NO:98)	6	GTGCG (SEQ ID NO:99)	JK2	-7	TTTGG (SEQ ID NO:100)
1.19. 2	A3.0	-3	TTACCC (SEQ ID NO:98)	6	GTGCG (SEQ ID NO:99)	JK2	-7	TTTGG (SEQ ID NO:100)

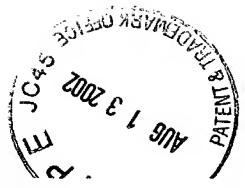
Figure 41A



1.19. 3	A230	-3	TTAACCC (SEQ ID NO:98)	6	GTGCAAG (SEQ ID NO:99)	JK2	-7	TTTTGG (SEQ ID NO:100)
6.4.1	A27/A27A	-3	CTGCAAC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.2	A27/A27A	-3	CTGCAAC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTGCAAC (SEQ ID NO:101)	6	GTGCAAG (SEQ ID NO:102)	JK2	-7	TTTTGG (SEQ ID NO:103)

Figure 41B

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF
Appl. No.: 10/041,860 Art. Doc#: ABGENIX.051A
Corvalan et al.



Clone #	VH	#DEL	VH END	# N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	# N's	N Sequence	JH del	# JH	Segment
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	GAGAGA (SEQ ID NO:104)	D3-16	22	TATTATGATTAC GTTGGGGGA (SEQ ID NO:105)	14	ATTATCGGCC (SEQ ID NO:106)	TCTTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)	
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	GAGAGA (SEQ ID NO:104)	D3-16	22	TATTATGATTAC GTTGGGGGA (SEQ ID NO:105)	14	ATTATCGGCC (SEQ ID NO:106)	TCTTT (SEQ ID NO:106)	JH4B	-1	CTACTT (SEQ ID NO:107)	
1.6.1	DP-77/3-21	0	GAGAGA (SEQ ID NO:104)	0	GAGAGA (SEQ ID NO:104)	D3-16	22	TATTATGATTAC GTTGGGGGA (SEQ ID NO:105)	14	ATTATCGGCC (SEQ ID NO:106)	TCTTT (SEQ ID NO:106)	JH4B	-1.	CTACTT (SEQ ID NO:107)	
1.11.1	DP-42/3-53	-5	AGAGAA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	TCTTT (SEQ ID NO:110)	JH6B	-2	TACTACT (SEQ ID NO:111)	
1.11.2	DP-42/3-53	-5	AGAGAA (SEQ ID NO:108)	3	GGA	D4-17	10	ACGGTGACTA (SEQ ID NO:109)	5	CGAAT (SEQ ID NO:110)	TCTTT (SEQ ID NO:110)	JH6B	-2	TACTACT (SEQ ID NO:111)	
1.23.1	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT	D3-10	19	TTCGGGGAGTTA ATGT (SEQ ID NO:113)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:115)		
1.23.2	DP-73/5-51	0	GAGACA (SEQ ID NO:112)	18	TGTATCGTATTACT	D3-10	19	TTCGGGGAGTTA ATGT (SEQ ID NO:113)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:115)		

Figure 42A

AppL No.: 10/041,860 Atty Docket: ABGENLX.051A
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ANTEROSES DIRECTED TO PDGF AND USES THEREOF
30047960 * 08/2028



				#n			
1.6.1	A30	-3	TTACCC	0	0	JK4	0
			(SEQ ID NO:116)				GCTCACT
1.6.2	A30	-3	TTACCC	0	0	JK4	0
			(SEQ ID NO:116)				(SEQ ID NO:117)
1.6.3	A30	-3	TTACCC	0	0	JK4	0
			(SEQ ID NO:116)				GCTCACT
1.11.1	A3/A19/DPK	-4	AAACTC	0	0	JK4	0
			(SEQ ID NO:118)				(SEQ ID NO:117)
1.11.2	A3/A19/DPK	-4	AAACTC	0	0	JK4	-2
			(SEQ ID NO:118)				TCACTRTC
1.23.1	A30	-3	TTACCC	0	0	JK4	-2
			(SEQ ID NO:120)				TCACTRTC
1.23.2	A30	-3	TTACCC	0	0	JK1	0
			(SEQ ID NO:120)				GTGGAC

Figure 42B

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF
Covallan et al.
Appl. No.: 10/041,860 Atty Doc#: ABGENX.051A



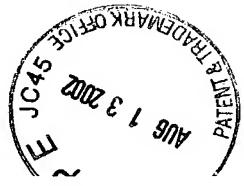
Clone #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTA(TACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTA(TACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D5-18	8	GGATACA (SEQ ID NO:122)	9	ATATGCTG (SEQ ID NO:123)	JH6B	-1	TTA(TACT (SEQ ID NO:124)
1.18	DP-16/1-8	1	CQAGAG (SEQ ID NO:125)	1	A	D8-18	19	GGGTATA CAGGGCT (SEQ ID NO:126)	4	GACA	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.26.1	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTA TGGTTCGG AGACTTATT ATAA	3	TGT	JH4B	-4	CTTTGA (SEQ ID NO:135)

Figure 43A



Clone #	VH	#DEL	VH END	#Ns	N Sequence	DH	Size of D	D Sequence	#Ns	N Sequence	JH	#del	JH Segment
1.25.2	DP-73/5-51	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTAATTAA TGTTTCGG AGACTTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	-4	CTTGA (SEQ ID NO:134)
1.29	DP-73/5-51	0	GAGACA (SEQ ID NO:135)	1	C	D5-12	21	GTTGATGT AGGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA (SEQ ID NO:139)	2	TC	D21-9	18	ATTACTAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	-4	CTACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG (SEQ ID NO:143)	2	GA	D21-9	19	TATTACTA TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	-4	CTACTA (SEQ ID NO:146)
1.39.1	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT AtaaTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:150)
1.39.2	DP-73/5-51	0	GAGACA (SEQ ID NO:147)	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATTACT AtaaTCG GGGAGTTA TTATAAC (SEQ ID NO:149)	2	GT	JH4B	-4	CTTGA (SEQ ID NO:150)

Figure 43B



CLONE #	V/H	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
1.40.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.40.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:152)	2	CA	JH6B	-6	ACTACT (SEQ ID NO:153)
1.45	DP-15/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-6	ACTACT (SEQ ID NO:156)
1.46.1	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GCTGGTA GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.46.2	DP-15/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGGT AGCTGCTA C (SEQ ID NO:158)	2	GG	JH6B	-6	ACTACT (SEQ ID NO:159)
1.48.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATGTTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.48.2	DP-14/1-18	1	CGAGAG	7	TGTTGAA	D21-9	20	TATTACTA	1	T	JH4B	0	ACTACT

Figure 43C



CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D Sequence	#N's	N Sequence	JH	#del	JH Segment	
			(SEQ ID NO:160)	(SEQ ID NO:161)			TGATGGTA (SEQ ID NO:162)					(SEQ ID NO:163)	
1.49.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTGGAA GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-6	TGGTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:168)	1	C	D3-16	31	TATGATTA CGTTGGAA GGAATTAT CGGTATA (SEQ ID NO:169)	5	CAGGG (SEQ ID NO:170)	JH5B	-6	TGGTC (SEQ ID NO:171)

Figure 43D

CLONE	VK	#del	Vk end	#n	N SEQ	JK	#del	JK end
1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)



CLONE	V _K	#del	V _K end	#n	N SEQ	J _K	#del	J _K end
1.17.2	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.17.3	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)
1.18	A30	3	TTACCC (SEQ ID NO:174)	0	0	JK3	0	ATTAC (SEQ ID NO:175)
1.24.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.24.2	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:177)
1.26.1	A30	3	TTACCC (SEQ ID NO:176)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.25.2	A30	3	TTACCC (SEQ ID NO:178)	0	0	JK1	0	GTGGAC (SEQ ID NO:179)
1.29	A3/A19/DPK	7	CTACAA (SEQ ID NO:180)	14	TCTCTCATG TGCGAG (SEQ ID NO:181)	JK2	7	TTTTGG (SEQ ID NO:182)
1.33	A20/DPK4	3	TGCCCC (SEQ ID NO:183)	0	0	JK4	0	GCTCAC (SEQ ID NO:184)
1.38.1	A20/DPK4	3	TGCCCC (SEQ ID NO:185)	0	0	JK1	0	GTGGAC (SEQ ID NO:186)
1.38.1	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)

Figure 43E

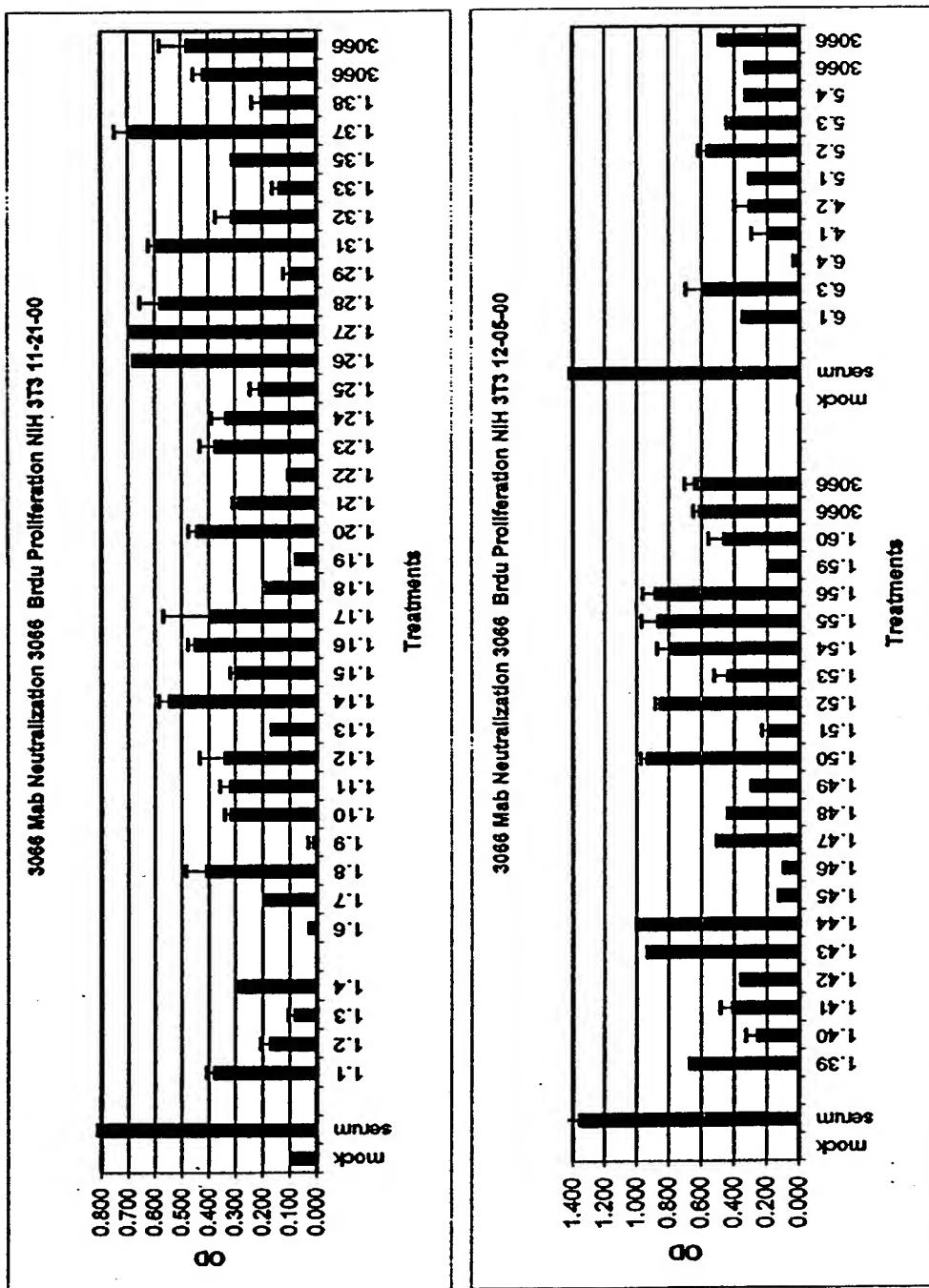


CLONE	VK	#del	VK end	#h	N SEQ	JK	# del	JK end
1.39.2	A30	3	TTACCC (SEQ ID NO:187)	0	0	JK1	0	GTGGAC (SEQ ID NO:188)
1.45	A20/DPK4	3	TGCCCC (SEQ ID NO:189)	0	0	JK3	0	ATTCAC (SEQ ID NO:190)
1.46.1	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.46.2	A30	0	CCCTCC (SEQ ID NO:191)	0	0	JK1	-3	GACGTT (SEQ ID NO:192)
1.48.1	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.48.2	L5/DPK5V	1	TCCCTC (SEQ ID NO:193)	0	0	JK1	-2	GGACGTT (SEQ ID NO:194)
1.49.1	A3/A19/DPK	5	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.49.2	A3/A19/DPK	6	CAAACT (SEQ ID NO:195)	0	0	JK5	-1	ATCACC (SEQ ID NO:196)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:197)	1	T	JK3	0	ATTCAC (SEQ ID NO:198)

Figure 43F



FIGURE 44



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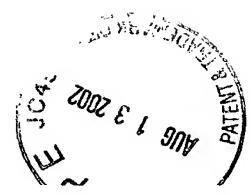
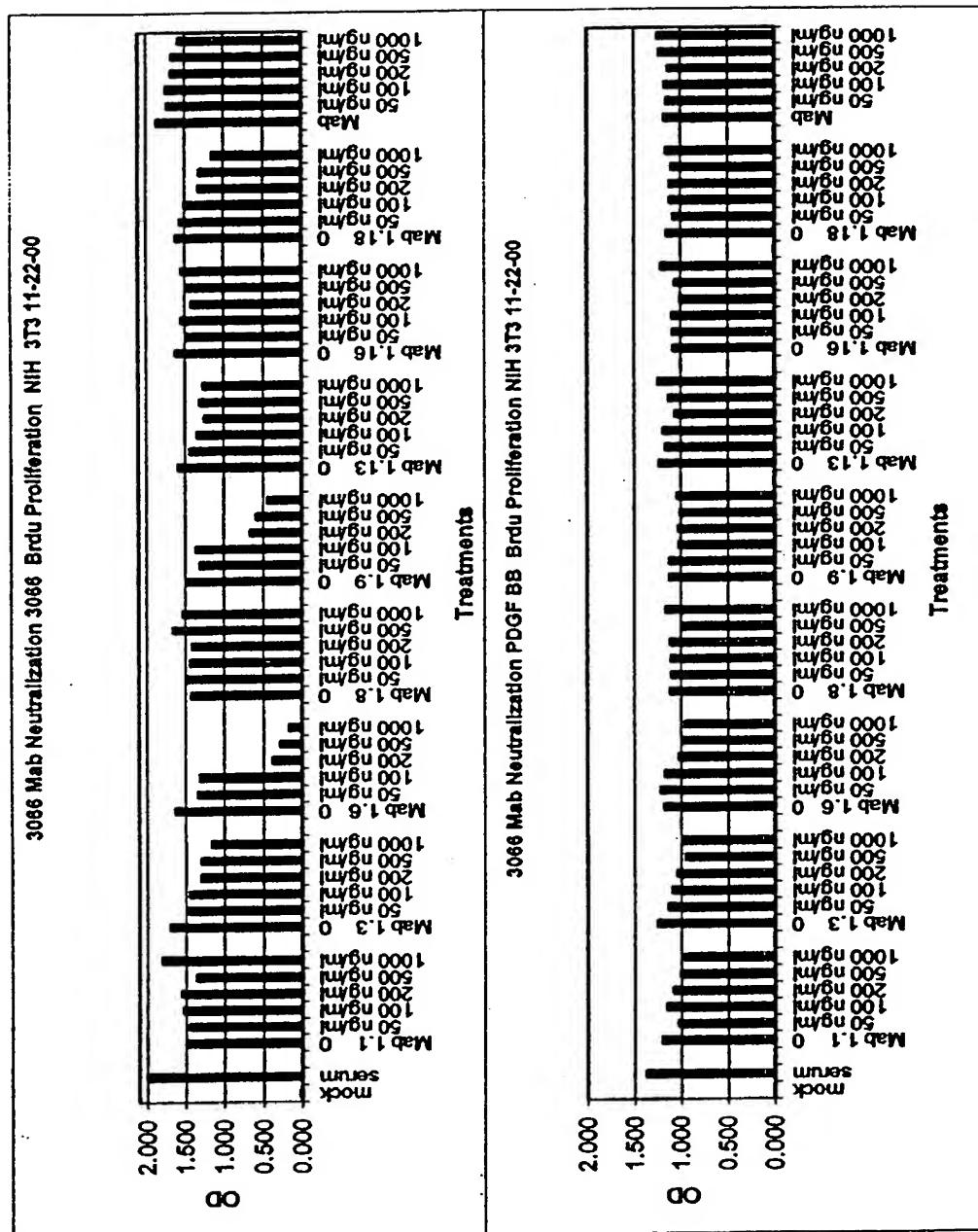


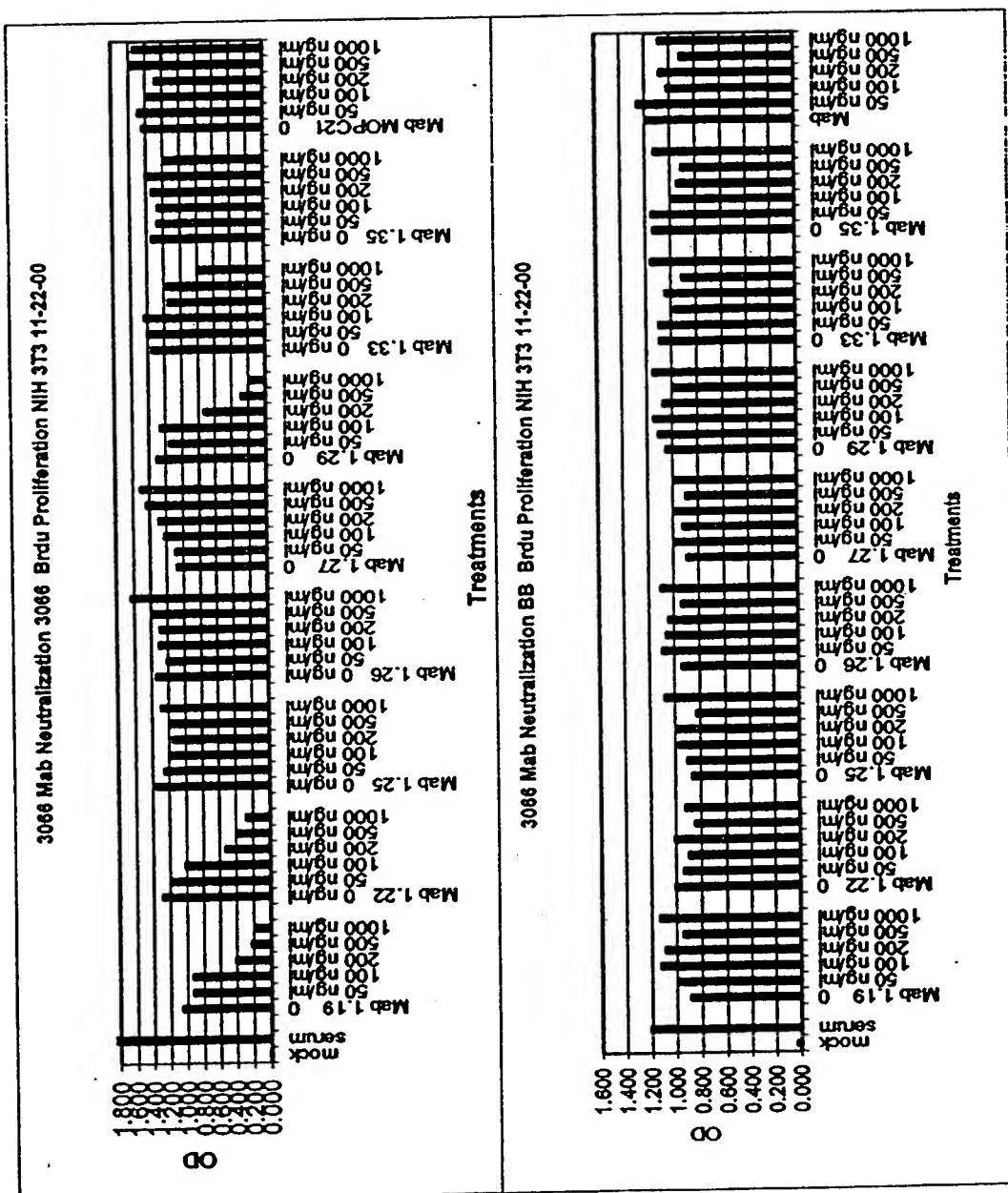
FIGURE 45



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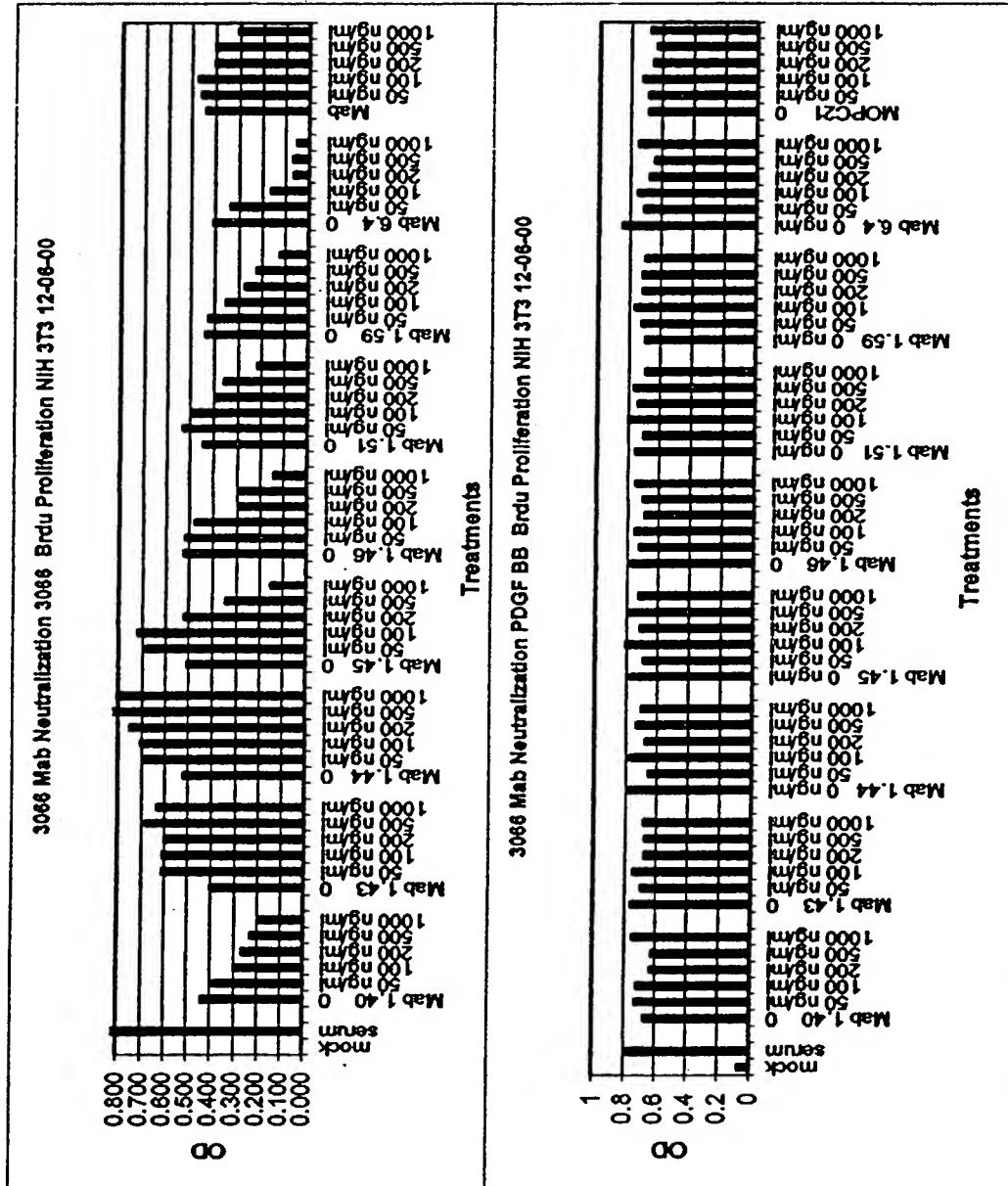
AUG 13 2002 EJC45
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Figure 46



ANTIBODIES DIRECTED TO PGCDF AND USES THEREOF
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FIGURE 47



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AUG 13 2002

FIGURE 48

1.19 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
6.4 H	1	Q	A	A V V	K	T	D N	T Q	WINPNSGN D	60	
1.18 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
1.40 H	1	Q	A	A V V	K	T	T D N	T Q	WMNPNSGN G	60	
1.45 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGN G	60	
1.46 H	1	Q	A	A V V	K	S	D N	T Q	WMNPNNGN G	60	
1.49 H	1	Q	A	A V V	K	T	D N	T Q	WMNPNSGD G	60	
1.33 H	1	Q	A	A V V	K	T	G S	P Q	WISAYNGN N	60	
1.48 H	1	Q	A	A V V	K	T	G S	P Q	WISAYNGN N	60	
1.6 H	1	E	E	GGLV	G LRL	A	FN RT	NMN	P K	VSSISSSSNIY	60
1.17 H	1	Q	E	GG VQ	K LRL	A	FT S	GMH	P K	VAVIWYDGNSNKY	60
1.24 H	1	Q	E	GG VQ	R LRL	A	FS S	GMH	P K	VADIWYDGNSNKY	60
1.38 H	1	Q	E	GG VQ	R LRL	A	FT S	GMH	P K	VAIIWYDGNDKY	60
1.11 H	1	E	GGLIQ	G LRL	A	FTVS	NYMS	P K	VSVIYSGGS- Y	59	
1.23 H	1	E	A	E L I	EG	S	W G	MP K	IIYPGDSD R	60	
1.25 H	1	E	A	E L I	KG	R	W G	MP K	IIYPGDSD R	60	
1.29 H	1	E	A	E L I	KG	S	W G	MP K	IIYPGDSD R	60	
1.39 H	1	E	T	E L I	KG	R	W G	MP K	IIYPGDSD R	60	
1.51 H	1	E	A	E L I	KG	S	W G	MP K	IIYPGDSDAK	60	
							[CDR1]		[CDR2]		

1.19 H	61	QKF	V MTRNT	I	MELS	SE	V	--DVM-ITFGGVIVH-YGM V	116
6.4 H	61	QKF	V MTRDT	I	MELS	SE	I V	--GFG-YSYN-YD -YGM V	115
1.18 H	61	QKF	V MTRNT	I	MELS	SE	V	--EG--IAVAGTY YYGM V	116
1.40 H	61	QKF	V MTRNT	L	MELS	SE	V	--DIV-VVVAATN -NGM V	116
1.45 H	61	QKF	V MTRNT	I	MELS	SE	V	--GSG-YSYG-YD -YGM V	115
1.46 H	61	QKF	V MTRNT	I	MELS	SE	V	--DIV-VVVTATD -YGM V	116
1.49 H	61	QKF	V MTRNT	I	MELS	SE	V F	--MRD-IVATSYY FYGM V	117
1.33 H	61	QKL	V MTTDT	T	MELR	SD	V	--DHY-YDSSDYL YYGL V	117
1.48 H	61	QKL	V MTTDT	T	MELR	SD	V	DVEYY-YDGSGYY FDY----	115
1.6 H	61	DSVK	F ISRDNAKNSL	LQMN	AE	V	DIMI---TFG-GIIASFYF Y	116	
1.17 H	61	DSVK	F ISRDN	KN L	LQMN	AE	V	DQGY---RYA-GY DYGM V	116
1.24 H	61	DSVK	F ISRDN	KN L	LQMN	AE	V	DQGY---SYG-YV DYGM V	116
1.38 H	61	DSVK	F VSRDN	KN L	LQMN	AE	V	GYYYD--SSD-YL YYGM V	117
1.11 H	60	DSVK	F ISRDN	KN L	LQMN	AE	V	GTVTT-----N YYGM V	110
1.23 H	61	SPSF	QV ISADK	I	LQWS	KAS	M	HVSY---YYVSGS -NVF Y	116
1.25 H	61	SPSF	QV ISADK	I	LQWS	KAS	M	HGSY---YYGSET -NVF Y	116
1.29 H	61	SPSF	QA ISADK	I	LQWS	KAS	M	HVDVGATIGGYYY -HGM V	119
1.39 H	61	SPSF	QV ISADK	I	LQWS	KAS	M	HGSY---YYNSGS -NVF Y	116
1.51 H	61	SPSF	QV ISADK	I	LQWS	KAS	M	HYDY---VWRNYR T-GWF P	116
							[CDR3]		



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FIGURE 48 (CONT)

1.19 H	117	T	126
6.4 H	116	T	125
1.18 H	117	T	126
1.40 H	117	T	126
1.45 H	116	T	125
1.46 H	117	T	126
1.49 H	118	T	127
1.33 H	118	T	127
1.48 H	116	L	125
1.6 H	117	L	126
1.17 H	117	T	126
1.24 H	117	T	126
1.38 H	118	T	127
1.11 H	111	T	120
1.23 H	117	L	126
1.25 H	117	L	126
1.29 H	120	T	129
1.39 H	117	L	126
1.51 H	117	L	126



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FIGURE 49

1.48 L 1	V	T	SS-----W A	A KL	I Q 55
1.49 L 1	V	L PVTP EPAS S	S SLLHSNGYNY D LL	QS QL	LG SRA 60
1.11 L 1	V	L PVTP EPAS S	S SLLQSNGYNY D L	QS QL	LG NRA 60
1.29 L 1	V	L PVTP EPAS S	S SLLHSNGYNY D L	QS QL	LG NRA 60
1.45 L 1			N SN-----D A	V KL	T Q 55
1.33 L 1			T SN-----Y A	V KL	T Q 55
1.38 L 1			T SN-----Y A	V NL	T Q 55
6.4 L 1	E VL	GT L P E A LS	SVSSS----Y A	QA RL	T SRA 56
1.51 L 1	E VL	GT L P E A LS	SVSSS----Y A	QA RL	G NRA 56
1.19 L 1			T RN-----D G	A KR	S Q 55
1.18 L 1			T RN-----D G	A KR	S Q 55
1.16 L 1			T RN-----D G F	A KR	S Q 55
1.23 L 1			T RN-----D G I	A KR	S Q 55
1.25 L 1			T RN-----D G	A KR	S Q 55
1.39 L 1			T RN-----D G	A KR	S Q 55
1.17 L 1			T RN-----D G	A KR	S Q 55
1.24 L 1			T RN-----D G	A KR	S Q 55
1.46 L 1			T RN-----D G	A KR	F S P 55
[CDR1]				[CDR2]	

1.48 L 56	D	F S	Q SN F R -	Q	107
1.49 L 61	D	K RVEA	VGV M TLQTIT--	Q RL	111
1.11 L 61	D	K RVEA	VGV M ALQTLT--	G	111
1.29 L 61	D	K RVEAD	VGV M ALQSLMCS	Q L	113
1.45 L 56	L	D	V T QKYN A F -	P D	107
1.33 L 56		D	V T QKYN A L -	G	107
1.38 L 56		D S	V A QKCN A W -	Q T	107
6.4 L 57	T I D	D	R E F V Q YG S CS-	Q L	108
1.51 L 57	T I D	D	R E F V Q YG SLF -	P D	108
1.19 L 56		D	F T L HN D CS-	Q L R	107
1.18 L 56		E	F T F L HN Y F -	P D	107
1.16 L 56		E	F T L HN Y L -	G	107
1.23 L 56	R	E	F T L HN Y W -	Q	107
1.25 L 56		E	F T L HN Y W -	Q	107
1.39 L 56		E	F T L HN Y L -	G	107
1.17 L 56		E	F T L HN Y W -	Q	107
1.24 L 56		E	F T L HSGY P -	Q	107
1.46 L 56		E	[CDR3]		



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FIGURE 50

1.19 H 1				I	D	60
6.4 H 1						60
1.18 H 1						60
1.40 H 1				T		60
1.45 H 1						60
1.46 H 1				S		60
1.49 H 1					N	60
					D	60
				[CDR1]	[CDR2]	
1.19 H 61					DVMITFGGG-VIVH	119
6.4 H 61				I	V GFGYSYN--YD	118
1.18 H 61					EGIAVAGT-YY	119
1.40 H 61				L	DIVVVVAA-TN N	119
1.45 H 61					GSGYSYG--YD	118
1.46 H 61					DIVVVVTA-TD	119
1.49 H 61				F	MRDIVATSYYY F	120
					[CDR3]	
1.19 H 120						
6.4 H 119						
1.18 H 120						
1.40 H 120						
1.45 H 119						
1.46 H 120						
1.49 H 121						



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FIGURE 51

1.33 H 1
1.48 H 1

[CDR1]

60
60

1.33 H 61
1.48 H 61

[]

--DH S D L YY GLDV 118
DVEY G G Y FD ---- 116
[CDR3]

1.33 H 119 T 127
1.48 H 117 L 125



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FIGURE 52

1.17 H 1	K	T	V	SN	60
1.24 H 1	R	S	D	SN	60
1.38 H 1	R	T	I	ND	60
		[CDR1]		[CDR2]	
1.17 H 61	I		DQG -RYAGY	D	119
1.24 H 61	I		DQG -SYGYV	D	119
1.38 H 61	V		GYY DSSDYL	Y	120
			[CDR3]		
1.17 H 120		126			
1.24 H 120		126			
1.38 H 121		127			



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FIGURE 53

1.23 H 1
1.25 H 1
1.29 H 1
1.39 H 1
1.51 H 1

T

E S 60
R 60
S 60
R 60
S AK 60
[CDR1] [CDR2]

1.23 H 61
1.25 H 61
1.29 H 61
1.39 H 61
1.51 H 61

A

]

VS YYVSG---S NV Y 117
GS YYGSE---T NV Y 117
VDVGATIGGYYY HGM V 120
GS YYNSG---S NV Y 117
YD VWRNY---R TGW P 117
[CDR3]

1.23 H 118
1.25 H 118
1.29 H 121 T 129
1.39 H 118
1.51 H 118

126
126
126
126
126



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FIGURE 54

1.49 L 1
1.11 L 1
1.29 L 1

H L S 60
Q Q N 60
H Q N 60
[CDR1] [CDR2]

1.49 L 61
1.11 L 61
1.29 L 61

]

E T TIT-- Q RL 111
E A TLT-- G KV 111
D A SLMCS Q KL 113
[CDR3]



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FIGURE 55

1.45 L 1	N	D	K	L	60
1.33 L 1	T	Y	K	S	60
1.38 L 1	T	Y	N	S	60

[CDR1]

[CDR2]

1.45 L 61	T	T	F	P	K	D	107	
1.33 L 61	T	Y	L	G	K	E	107	
1.38 L 61	S	A	C	W	Q	T	E	107

[CDR3]



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FIGURE 56

6.4 L 1
1.51 L 1

[CDR1]

AT S 60
GA N 60
[CDR2]

6.4 L 61
1.51 L 61

PCS Q LE 108
LFT P VD 108
[CDR3]



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FIGURE 57